

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Yi Li and Mark D. Adams
- (ii) TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
Cecchi, Stewart & Olstein
- (B) STREET: 6 Becker Farm Road
- (C) CITY: Roseland
- (D) STATE: NJ
- (E) COUNTRY: US
- (F) ZIP: 07068-1739

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: WordPerfect 5.1

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/465,971
- (B) FILING DATE: 06-JUN-1995
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: MULLINS, J.G.
- (B) REGISTRATION NUMBER: 33073
- (C) REFERENCE/DOCKET NUMBER: 325800-453 (PF187)

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 201-994-1700
- (B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2764 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATTACAGGT AACATTCTGA AATTGAACTA AACAGTAAAT TCTGTTGAAA TGTTTTTCAAA	60
GAGGCAAAAT ATTATATTGG AATCAATGAA GAAAGTAAAT TATCTTGGCT AATTTTATTA	120
GTGGTAATTG TAGTGAAAGG TTTTCCTAAA TATTATAAGC AAATTCCTTT TCTCCCCCGT	180
CTCAAATGAA AGGAAATGGG GGTAATTAA TCTGACTGTG ATTGGTTTTG TTTTATGCTG	240
ATCTTGAAAG CTTGATGTTG CTGCTGCTCC TCATACAGTA CAGATCAGTT GTGTGGGGTG	300
CTATTGAGGG TAGCCGTGAA TAGTGGTGCC AGTAGGGGTG GAGCGGGAGG GATGATGCCA	360
GCCTGAGCTA GCCAGGTTCT TTGATTAGGG CATTGGATGT GAAATGTAAA ATGCTCTCTC	420
CTTTTCCTCT ATCAGCTGTT CAGAGGAGAC TCATTACAAC TCCTGCTGAA GCTCCTAATC	480
TTCTTCCCTT CTCTTCTACC CTTTCCCCCT ACCCTCACTT GGCCTGAAGA CGTTCTCCCC	540
AGAGTTTACC TTGCTCCCCT GGTGCTATGT GTATGGTGAA CCTGGCACTA TGGCCGCGTC	600
TGGGACTGGC CAGACAACTG CTGCTGGCTC TCCTTATTCC AGGAAGGATT TAAAGGGGAA	660
TTGCACTGCA GGCAATGCAC CAGAGCAGCA GCATCAGGAG CTTGGGGAGT AAGGCTCCTC	720
TGGCATTATT ACACACATGC AAAGCTGACC GCAATGACAG CAGCTGCTTC TTTGAACTGT	780
TGGCAGCAGC CAAGCGGCAG CATGAAGTGA CAGATCACTC CTGAGCTCAA G ATG AAC	837
	Met Asn
TCC ACC TTG GAT GGT AAT CAG AGC AGC CAC CCT TTT TGC CTC TTG GCA	885
Ser Thr Leu Asp Gly Asn Gln Ser Ser His Pro Phe Cys Leu Leu Ala	
5 10 15	
TTT GGC TAT TTG GAA ACT GTC AAT TTT TGC CTT TTG GAA GTA TTG ATT	933
Phe Gly Tyr Leu Glu Thr Val Asn Phe Cys Leu Leu Glu Val Leu Ile	
20 25 30	
ATT GTC TTT CTA ACT GTA TTG ATT ATT TCT GGC AAC ATC ATT GTG ATT	981
Ile Val Phe Leu Thr Val Leu Ile Ile Ser Gly Asn Ile Ile Val Ile	
35 40 45 50	
TTT GTA TTT CAC TGT GCA CCT TTG TTG AAC CAT CAC ACT ACA AGT TAT	1029
Phe Val Phe His Cys Ala Pro Leu Leu Asn His His Thr Thr Ser Tyr	
55 60 65	
TTT ATC CAG ACT ATG GCA TAT GCT GAC CTT TTT GTT GGG GTG AGC TGC	1077
Phe Ile Gln Thr Met Ala Tyr Ala Asp Leu Phe Val Gly Val Ser Cys	
70 75 80	
GTG GTC CCT TCT TTA TCA CTC CTC CAT CAC CCC CTT CCA GTA GAG GAG	1125
Val Val Pro Ser Leu Ser Leu Leu His His Pro Leu Pro Val Glu Glu	
85 90 95	
TCC TTG ACT TGC CAG ATA TTT GGT TTT GTA GTA TCA GTT CTG AAG AGC	1173
Ser Leu Thr Cys Gln Ile Phe Gly Phe Val Val Ser Val Leu Lys Ser	
100 105 110	
GTC TCC ATG GCT TCT CTG GCC TGT ATC AGC ATT GAT AGA TAC ATT GCC	1221
Val Ser Met Ala Ser Leu Ala Cys Ile Ser Ile Asp Arg Tyr Ile Ala	
115 120 125 130	

ATT ACT AAA CCT TTA ACC TAT AAT ACT CTG GTT ACA CCC TGG AGA CTA	1269
Ile Thr Lys Pro Leu Thr Tyr Asn Thr Leu Val Thr Pro Trp Arg Leu	
135 140 145	
CGC CTG TGT ATT TTC CTG ATT TGG CTA TAC TCG ACC CTG GTC TTC CTG	1317
Arg Leu Cys Ile Phe Leu Ile Trp Leu Tyr Ser Thr Leu Val Phe Leu	
150 155 160	
CCT TCC TTT TTC CAC TGG GGC AAA CCT GGA TAT CAT GGA GAT GTG TTT	1365
Pro Ser Phe Phe His Trp Gly Lys Pro Gly Tyr His Gly Asp Val Phe	
165 170 175	
CAG TGG TGT GCG GAG TCC TGG CAC ACC GAC TCC TAC TTC ACC CTG TTC	1413
Gln Trp Cys Ala Glu Ser Trp His Thr Asp Ser Tyr Phe Thr Leu Phe	
180 185 190	
ATC GTG ATG ATG TTA TAT GCC CCA GCA GCC CTT ATT GTC TGC TTC ACC	1461
Ile Val Met Met Leu Tyr Ala Pro Ala Ala Leu Ile Val Cys Phe Thr	
195 200 205 210	
TAT TTC AAC ATC TTC CGC ATC TGC CAA CAG CAC ACA AAG GAT ATC AGC	1509
Tyr Phe Asn Ile Phe Arg Ile Cys Gln Gln His Thr Lys Asp Ile Ser	
215 220 225	
GAA AGG CAA GCC CGC TTC AGC AGC CAG AGT GGG GAG ACT GGG GAA GTG	1557
Glu Arg Gln Ala Arg Phe Ser Ser Gln Ser Gly Glu Thr Gly Glu Val	
230 235 240	
CAG GCC TGT CCT GAT AAG CGC TAT GCC ATG GTC CTG TTT CGA ATC ACT	1605
Gln Ala Cys Pro Asp Lys Arg Tyr Ala Met Val Leu Phe Arg Ile Thr	
245 250 255	
AGT GTA TTT TAC ATC CTC TGG TTG CCA TAT ATC ATC TAC TTC TTG TTG	1653
Ser Val Phe Tyr Ile Leu Trp Leu Pro Tyr Ile Ile Tyr Phe Leu Leu	
260 265 270	
GAA AGC TCC ACT GGC CAC AGC AAC CGC TTC GCA TCC TTC TTG ACC ACC	1701
Glu Ser Ser Thr Gly His Ser Asn Arg Phe Ala Ser Phe Leu Thr Thr	
275 280 285 290	
TGG CTT GCT ATT AGT AAC AGT TTC TGC AAC TGT GTA ATT TAT AGT CTC	1749
Trp Leu Ala Ile Ser Asn Ser Phe Cys Asn Cys Val Ile Tyr Ser Leu	
295 300 305	
TCC AAC AGT GTA TTC CAA AGA GGA CTA AAG CGC CTC TCA GGG GCT ATG	1797
Ser Asn Ser Val Phe Gln Arg Gly Leu Lys Arg Leu Ser Gly Ala Met	
310 315 320	
TGT ACT TCT TGT GCA AGT CAG ACT ACA GCC AAC GAC CCT TAC ACA GTT	1845
Cys Thr Ser Cys Ala Ser Gln Thr Thr Ala Asn Asp Pro Tyr Thr Val	
325 330 335	
AGA AGC AAA GGC CCT CTT AAT GGA TGT CAT ATC TGAAGTGGCT CAGTTACGGG	1898
Arg Ser Lys Gly Pro Leu Asn Gly Cys His Ile	
340 345	
GTTCCTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT ATTTTATCTC TAAGTATTCC	1958
TAATTCACCTA GGAAATCTGG GACAGAATAC TTTGACTCTA AACAAATAGCA TACAAATTAT	
2018	
TCGTATGGAT ACCTTCTAAG TTTGTAGAAA TGGTTTTCCC AAGTGCTTGT GAATTAGAAG	2078

ACTCAAGATC ATGAAGACAA ATTGCTCTTG CTCTCAATTT TTGAAATGTC TTGGAAATGA 2138
CTACAGTTCT CAGATTTAAA ATGAATAAAG CCATATCTAA CACCTCTTTC CAGCTGGCAT 2198
GACTGAACCT GAGTGTGAAA AGCGTCAGCA TTTTAAAAAG TCATCACTTT CTTGTCACIT 2258
TCTGGGCTCT TTCCAGCTAT TTGGGCGTCA TATGCAATTG ATTTCTTCTA ACGGAATAGT 2318
AAAATATAAA TGAAAAGGTT TTAGAAATTA CTTTTTATGT ATGCCAAAGC ATAACCTACAC 2378
TGCAAGTTTC AACACTGTCA TTTAGAAAGC CAAATGTTCT GTGTTTTATF CTCTTGAGAG 2438
AATTCTCAGT AGGGTGAATA ATGTGAACAC ATAAACATTA ATTTTAGAAT TTTACAGTGA 2498
ACCATGAAGC AAAAGTGCAA TCAAATTATA CAATTTATGA AAAACTGAGC TACTTTTTGT 2558
GCCATGCTTC ACAGAGATCT AAAGATATGT GTGCGTAGAA GTAATCGTGT AGTACTTTTG 2618
CCCATGCCIT TGTGTTATGT CTATATTTAG AATATCTGAA TTGTTAGATT TCTCTTTTAC 2678
AGCAAAATGT GCTTAAGCTA AAAAGTAATT CAGGGAATTC GATATCAAGC TTATCGATAC 2738
CGTCGACCTC GAGGGGGGGC CCGGTA 2764

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asn	Ser	Thr	Leu	Asp	Gly	Asn	Gln	Ser	Ser	His	Pro	Phe	Cys	Leu
				5				10						15	
Leu	Ala	Phe	Gly	Tyr	Leu	Glu	Thr	Val	Asn	Phe	Cys	Leu	Leu	Glu	Val
			20					25					30		
Leu	Ile	Ile	Val	Phe	Leu	Thr	Val	Leu	Ile	Ile	Ser	Gly	Asn	Ile	Ile
			35				40					45			
Val	Ile	Phe	Val	Phe	His	Cys	Ala	Pro	Leu	Leu	Asn	His	His	Thr	Thr
			50			55					60				
Ser	Tyr	Phe	Ile	Gln	Thr	Met	Ala	Tyr	Ala	Asp	Leu	Phe	Val	Gly	Val
					70					75					80
Ser	Cys	Val	Val	Pro	Ser	Leu	Ser	Leu	Leu	His	His	Pro	Leu	Pro	Val
				85				90						95	
Glu	Glu	Ser	Leu	Thr	Cys	Gln	Ile	Phe	Gly	Phe	Val	Val	Ser	Val	Leu
			100					105					110		
Lys	Ser	Val	Ser	Met	Ala	Ser	Leu	Ala	Cys	Ile	Ser	Ile	Asp	Arg	Tyr
			115				120					125			
Ile	Ala	Ile	Thr	Lys	Pro	Leu	Thr	Tyr	Asn	Thr	Leu	Val	Thr	Pro	Trp
			130			135					140				
Arg	Leu	Arg	Leu	Cys	Ile	Phe	Leu	Ile	Trp	Leu	Tyr	Ser	Thr	Leu	Val
					150					155					160
Phe	Leu	Pro	Ser	Phe	Phe	His	Trp	Gly	Lys	Pro	Gly	Tyr	His	Gly	Asp
				165				170						175	
Val	Phe	Gln	Trp	Cys	Ala	Glu	Ser	Trp	His	Thr	Asp	Ser	Tyr	Phe	Thr
			180					185						190	

Leu	Phe	Ile	Val	Met	Met	Leu	Tyr	Ala	Pro	Ala	Ala	Leu	Ile	Val	Cys
		195					200					205			
Phe	Thr	Tyr	Phe	Asn	Ile	Phe	Arg	Ile	Cys	Gln	Gln	His	Thr	Lys	Asp
	210					215				220					
Ile	Ser	Glu	Arg	Gln	Ala	Arg	Phe	Ser	Ser	Gln	Ser	Gly	Glu	Thr	Gly
225					230					235					240
Glu	Val	Gln	Ala	Cys	Pro	Asp	Lys	Arg	Tyr	Ala	Met	Val	Leu	Phe	Arg
				245					250					255	
Ile	Thr	Ser	Val	Phe	Tyr	Ile	Leu	Trp	Leu	Pro	Tyr	Ile	Ile	Tyr	Phe
			260					265					270		
Leu	Leu	Glu	Ser	Ser	Thr	Gly	His	Ser	Asn	Arg	Phe	Ala	Ser	Phe	Leu
		275					280					285			
Thr	Thr	Trp	Leu	Ala	Ile	Ser	Asn	Ser	Phe	Cys	Asn	Cys	Val	Ile	Tyr
	290					295					300				
Ser	Leu	Ser	Asn	Ser	Val	Phe	Gln	Arg	Gly	Leu	Lys	Arg	Leu	Ser	Gly
305					310					315					320
Ala	Met	Cys	Thr	Ser	Cys	Ala	Ser	Gln	Thr	Thr	Ala	Asn	Asp	Pro	Tyr
				325					330					335	
Thr	Val	Arg	Ser	Lys	Gly	Pro	Leu	Asn	Gly	Cys	His	Ile			
			340					345							

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Asn	Ser	Thr	Leu	Xaa	Asp	Gly	Asn	Gln	Ser	Ser	His	Pro	Phe	Cys
				5					10					15	
Leu	Leu	Ala	Phe	Gly	Tyr	Leu	Glu	Thr	Val	Asn	Phe	Cys	Leu	Leu	Glu
		20						25					30		
Val	Leu	Ile	Ile	Val	Xaa	Xaa	Xaa	Xaa	Phe	Leu	Thr	Val	Leu	Ile	Ile
		35					40					45			
Ser	Gly	Asn	Ile	Ile	Val	Ile	Phe	Val	Phe	His	Cys	Ala	Pro	Leu	Leu
	50					55					60				
Asn	His	His	Thr	Thr	Ser	Tyr	Phe	Ile	Gln	Thr	Met	Ala	Tyr	Ala	Asp
65					70					75					80
Leu	Phe	Val	Gly	Val	Ser	Cys	Val	Val	Pro	Ser	Leu	Ser	Leu	Leu	His
			85						90					95	
His	Pro	Leu	Pro	Xaa	Xaa	Val	Glu	Glu	Ser	Leu	Thr	Cys	Gln	Ile	Phe
		100						105					110		
Gly	Phe	Val	Val	Ser	Val	Leu	Lys	Ser	Val	Ser	Met	Ala	Ser	Leu	Ala
		115					120					125			
Cys	Ile	Ser	Ile	Asp	Arg	Tyr	Ile	Ala	Ile	Thr	Lys	Pro	Leu	Thr	Tyr
	130					135					140				
Asn	Thr	Leu	Val	Thr	Pro	Trp	Arg	Leu	Arg	Leu	Cys	Ile	Phe	Leu	Ile
145					150					155					160
Trp	Leu	Tyr	Ser	Thr	Leu	Val	Phe	Leu	Pro	Ser	Phe	Phe	His	Trp	Gly
			165						170					175	
Lys	Pro	Gly	Tyr	His	Gly	Asp	Val	Phe	Gln	Trp	Cys	Ala	Glu	Ser	Trp
		180						185					190		
Xaa	Xaa	Xaa	His	Thr	Asp	Ser	Tyr	Phe	Thr	Leu	Phe	Ile	Val	Met	Met
		195					200						205		

Leu	Tyr	Ala	Pro	Ala	Ala	Leu	Ile	Val	Cys	Phe	Thr	Tyr	Phe	Asn	Ile
210						215					220				
Phe	Arg	Ile	Cys	Gln	Gln	His	Thr	Lys	Asp	Ile	Ser	Glu	Arg	Xaa	Xaa
225				230					235						240
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gln	Ala	Arg	Phe	Ser
				245					250					255	
Ser	Gln	Ser	Gly	Xaa	Xaa	Xaa	Xaa	Glu	Thr	Gly	Glu	Val	Gln	Ala	Cys
			260					265					270		
Pro	Asp	Lys	Arg	Tyr	Ala	Met	Val	Leu	Phe	Arg	Ile	Thr	Ser	Val	Phe
		275					280					285			
Tyr	Ile	Leu	Trp	Leu	Pro	Tyr	Ile	Ile	Tyr	Phe	Leu	Leu	Glu	Ser	Ser
	290					295					300				
Thr	Gly	His	Ser	Asn	Arg	Phe	Ala	Ser	Phe	Leu	Thr	Thr	Trp	Leu	Ala
305				310					315						320
Ile	Ser	Asn	Ser	Phe	Cys	Asn	Cys	Val	Ile	Tyr	Ser	Leu	Ser	Asn	Ser
				325					330					335	
Val	Phe	Gln	Arg	Gly	Leu	Lys	Arg	Leu	Ser	Gly	Ala	Met	Cys	Thr	Ser
			340					345					350		
Cys	Ala	Ser	Gln	Thr	Thr										
			355												

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Gly	Ser	Leu	Gln	Pro	Asp	Ala	Gly	Asn	Ala	Ser	Trp	Asn	Gly	Thr
				5					10					15	
Glu	Ala	Pro	Gly	Gly	Gly	Ala	Arg	Ala	Thr	Pro	Tyr	Ser	Leu	Gln	Val
			20					25					30		
Thr	Leu	Thr	Leu	Val	Cys	Leu	Ala	Gly	Leu	Leu	Met	Leu	Leu	Thr	Val
			35				40					45			
Phe	Gly	Asn	Val	Leu	Val	Ile	Ile	Ala	Val	Phe	Thr	Ser	Arg	Ala	Leu
	50					55				60					
Lys	Ala	Pro	Gln	Asn	Leu	Phe	Leu	Val	Xaa	Ser	Leu	Ala	Ser	Ala	Asp
	65				70				75						80
Ile	Leu	Val	Ala	Xaa	Xaa	Thr	Leu	Val	Ile	Pro	Phe	Ser	Leu	Ala	Asn
			85						90					95	
Glu	Val	Met	Gly	Tyr	Trp	Tyr	Phe	Gly	Lys	Ala	Trp	Cys	Glu	Ile	Tyr
			100					105					110		
Leu	Ala	Leu	Asp	Val	Leu	Phe	Cys	Thr	Ser	Ser	Ile	Val	His	Leu	Cys
			115				120					125			
Ala	Ile	Ser	Leu	Asp	Arg	Tyr	Trp	Ser	Ile	Thr	Gln	Ala	Ile	Glu	Tyr
	130					135					140				
Asn	Leu	Lys	Arg	Thr	Pro	Arg	Arg	Ile	Lys	Ala	Ile	Ile	Ile	Thr	Val
	145				150				155						160
Trp	Val	Ile	Ser	Ala	Val	Ile	Ser	Phe	Pro	Pro	Leu	Ile	Ser	Ile	Glu
			165					170					175		
Lys	Lys	Gly	Xaa	Xaa	Gly	Gly	Gly	Gly	Pro	Gln	Pro	Ala	Glu	Pro	Arg
			180				185						190		
Cys	Glu	Ile	Asn	Asp	Gln	Lys	Trp	Tyr	Val	Ile	Ser	Ser	Cys	Ile	Gly
	195						200				205				
Ser	Phe	Phe	Ala	Pro	Cys	Leu	Ile	Met	Ile	Leu	Val	Tyr	Val	Arg	Ile
	210					215					220				

Tyr	Gln	Ile	Ala	Lys	Arg	Arg	Thr	Arg	Val	Pro	Pro	Ser	Arg	Arg	Gly
225					230					235					240
Pro	Asp	Ala	Val	Ala	Ala	Pro	Pro	Gly	Gly	Leu	Gln	Gly	Arg	Gly	Arg
				245					250					255	
Ser	Ala	Ser	Gly	Leu	Pro	Arg	Arg	Arg	Ala	Gly	Ala	Gly	Gly	Gln	Asn
			260					265					270		
Arg	Glu	Lys	Arg	Phe	Thr	Phe	Val	Leu	Ala	Val	Val	Ile	Gly	Val	Phe
		275					280					285			
Val	Val	Cys	Trp	Phe	Pro	Phe	Phe	Phe	Thr	Tyr	Thr	Leu	Thr	Ala	Val
	290					295					300				
Gly	Cys	Ser	Val	Pro	Arg	Thr	Leu	Phe	Lys	Phe	Phe	Phe	Trp	Phe	Gly
305					310					315					320
Tyr	Cys	Asn	Ser	Ser	Leu	Asn	Pro	Val	Ile	Tyr	Thr	Ile	Phe	Asn	His
			325						330					335	
Asp	Phe	Arg	Arg	Ala	Phe	Lys	Lys	Ile	Xaa	Xaa	Xaa	Leu	Cys	Arg	Gly
			340					345					350		
Asp	Arg	Lys	Arg	Ile	Val										
		355													

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGAATTCCT CCATGAACTC CACCTTGGAT

30

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGAAGCTTC GTCAGATATG ACATCCATT

29

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTCCAAGCTT GCCACCATGA ACTCCACCTT GGAT

34

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTAGCTCGAG TCAAGCGTAC TCTGGGACGT CGTATGGGTA GCAGATATGA CATCCATTAA

50

G

61

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGATCCCT CCATGAACTC CACCTTGGAT

30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGGATCCCG CTCAGATATG AGATCCATT

29